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**FIGURE 1**  
Map of a First IL-17 Receptor Like cDNA (SEQ ID No: 1)  
and Amino Acid (SEQ ID NO: 2)

```

1 ATAAAAGCGCAGCGTGCGGGTGGCCTGGATCCCGCGCAGTGGCCCGGCGATGTCGCTCGT 60
                                     M S L V -

61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120
   L L S L A A L C R S A V P R E P T V Q C -

121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGA 180
   G S E T G P S P E W M L Q H D L I P G D -

181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCAAT 240
   L R D L R V E P V T T S V A T G D Y S I -

241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCAC 300
   L M N V S W V L R A D A S I R L L K A T -

301 CAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTA 360
   K I C V T G K S N F Q S Y S C V R C N Y -

361 CACAGAGGCCCTTCCAGACTCAGACCAGACCCCTCTGGTGGTAAATGGACATTTTCCTACAT 420
   T E A F Q T Q T R P S G G K W T F S Y I -

421 CGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGC 480
   G F P V E L N T V Y F I G A H N I P N A -

481 AAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGA 540
   N M N E D G P S M S V N F T S P G C L D -

541 CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACAT 600
   H I M K Y K K K C V K A G S L W D P N I -

601 CACTGCTTGTAAGAAGAATGAGGAGACAGTAGAAGTGAAGTTCACAACCACTCCCCTGGG 660
   T A C K K N E E T V E V N F T T T P L G -

661 AAACAGATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGA 720
   N R Y M A L I Q H S T I I G F S Q V F E -

721 GCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGA 780
   P H Q K K Q T R A S V V I P V T G D S E -

781 AGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACA 840
   G A T V Q L T P Y F P T C G S D C I R H -

841 TAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAA 900
   K G T V V L C P Q T G V P F P L D N N K -

901 AAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGT 960
   S K P G G W L P L L L L S L L V A T W V -

961 GCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTC 1020
   L V A G I Y L M W R H E R I K K T S F S -

1021 TACCACCACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTT 1080
   T T T L L P P I K V L V V Y P S E I C F -

1081 CCATCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCGAGAAGTGAGGTCAT 1140
   H H T I C Y F T E F L Q N H C R S E V I -

1141 CCTCGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCAC 1200
   L E K W Q K K K I A E M G P V Q W L A T -

```

F03499-03499-260786

**SECRET**

— 4 —

[illegible]

```

1  .....MSLVLLSLAALCRSAVPREP 20
1  MGAARSPPSAVPGPLLGLLLLLLLGVLPAGGASLRLLDHRALVCSQPGLNC 50
21  TVQCGETGPSPEWMLQHDLI PGDLRLDRVEPVTTSVATGDYSILMNVS 70
   ||. . | . | . | | : || : : || . : |
51  TVK. .NSTCLDDSWIHPRNLTPSSPKDLQIQLFHAHTQOQDLFPVAHIEW 98
71  VLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWT 120
   |. ||| | . :. | | | | . . | : |
99  TLQTDASILYLEGAELSVL.QLNTNERLCVRFE...FLSKLRHHHRRWR 143
121  FSYIGFPVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYK 170
   |.: | |: | : |.: | | | | | | |
144  FTFSHFVVPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVT 193
171  KKCVKAGSLWDPNITACKKNEETVEVNFNTTTPGLNRYMALI.....QH 213
   |. . ||||| | | . | | | | : |
194  TPCMSSGSLWDPNITVETLEAHQLRVSF TLWNESTHYQILLTSFPHMENH 243
214  STIIGFSQVFEPHQKKQTRASVVI PVTGDSEGA...TVQLTPYFPTCGSD 260
   | : : | . . | | . . | | : | : | . |
244  SCFEHMHHPAPRPEEFHQRSNVTLTLRNLKGCCRHOVQIQPFFSSCLND 293
261  CIRHKGTVVLC PQ.TGVFPFLDNNKSKPGGWLPLLLLSLLVATWVLVAGI 309
   | : | | | | : | | : . . | : : | : | :
294  CLRHSAT.VSCPEMPDTPEPIPDYMWLVVYWF.ITGISILLVGSVILLIV 341
310  YLMWRHERIKKTSFSTTT.....LLP....PIKVLVVYPSE.ICF 344
   : || : | | | | : | | | : | : :
342  CMTWRLAGPGSEKYSDDTKYTDGLPAADLIPPLKPRKVWIIYSADHPLY 391
345  HHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK...KAAD 390
   : | : | | . | | : . . | . . | |
392  VDVVLKFAQFLLTACGTEVALDLLLEEQAISEAGVMTWVGRQKQEMVESNS 441
391  KVVFLLSNDVNSVCDGTGCKSEGSP.....SENSQDLFPLAFNLFCSD 433
   | : : | | : | . | | | | | | : |
442  KIIVLCSRGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPD 489
434  LRSQIHLHKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELL 480
   : | | | | | : | | | | : | | : |
490  FKRPAFCGTYYVCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDL 539
481  HVKQQVSAGKRSQACHDGCCSL*..... 503
540  EMFQPGRMHRVGELSGDNYLRSPGGROLRAALDRFRDWOVRCPDWFECEN 589

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FIGURE 3  
Map of a Second Human IL-17 Receptor Like cDNA (SEQ ID NO: 4)  
And Amino Acid (SEQ ID NO: 5) Sequences

1 ATAAAAGCGCAGCGTGC GG GTGGCCTGGATCCCGCGCAGTGGCCCGGCGATGTCGCTCGT 60  
M S L V -

61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGTTCAATG 120  
L L S L A A L C R S A V P R E P T V Q C -

121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGGAGA 180  
G S E T G P S P E W M L Q H D L I P G D -

181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTGCAACAGGGGACTATTCAAT 240  
L R D L R V E P V T T S V A T G D Y S I -

241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGTAAGGCCAC 300  
L M N V S W V L R A D A S I R L L K A T -

301 CAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCACAGCTGTGTGAGGCTGGAGTG 360  
K I C V T G K S N F Q S Y S C V R L E C -

361 CAGTGGTGC GATCATGGCTCGCTGCGACCTCAATCTTCTGGGCTCAAGCGATCGTTCTGC 420  
S G A I M A R C D L N L L G S S D R S A -

421 TTCAGCCTCCCGAGCGGCTGGGACTGCAGGCGTGGGCCACCAGACCTGGCTAATTTTTGT 480  
S A S R A A G T A G V G H Q T W L I F V -

481 AGTTTTTGTAGAGGGGGGTTTACC GTGTTGCTGGTCTTGAATTCCAGTGCTCAGGCGAT 540  
V F V E G G F T V L L V L N S S A Q A I -

541 CTGCCTGCCTCGGCTTCCCAAAGTGCTGGGATTACAGTGGACATTTTCTACATCGGCTT 600  
C L P R L P K V L G L Q W T F S Y I G F -

601 CCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGCAAATAT 660  
P V E L N T V Y F I G A H N I P N A N M -

661 GAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACAT 720  
N E D G P S M S V N F T S P G C L D H I -

721 AATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGC 780  
M K Y K K K C V K A G S L W D P N I T A -

781 TTGTAAGAAGAATGAGGAGACAGTAGAAGTGAAC T T C A C A A C C A C T C C C T G G G A A A C A G 840  
C K K N E E T V E V N F T T T P L G N R -

841 ATACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACA 900  
Y M A L I Q H S T I I G F S Q V F E P H -

901 CCAGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGC 960  
Q K K Q T R A S V V I P V T G D S E G A -

961 TACGGTGCAGCTGACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACATAAAGG 1020  
T V Q L T P Y F P T C G S D C I R H K G -

FIGURE 3

Figure 3 (continued)

1021 AACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAA 1080  
T V V L C P Q T G V P F P L D N N K S K -

1081 GCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGT 1140  
P G G W L P L L L L S L L V A T W V L V -

1141 GGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCAC 1200  
A G I Y L M W R H E R I K K T S F S T T -

1201 CACACTACTGCCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCA 1260  
T L L P P I K V L V V Y P S E I C F H H -

1261 CACAATTTGTTACTTCACTGAATTTCTTCAAACCATTGCAGAAGTGAGGTCATCCTCGA 1320  
T I C Y F T E F L Q N H C R S E V I L E -

1321 AAAGTGGCAGAAAAAGAAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAA 1380  
K W Q K K K I A E M G P V Q W L A T Q K -

1381 GAAGGCAGCAGACAAAGTCGTCTTCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGG 1440  
K A A D K V V F L L S N D V N S V C D G -

1441 TACCTGTGGCAAGAGCGAGGGCAGTCCCACTGAGAAGTCTCAAGACCTTCCCCCTTGC 1500  
T C G K S E G S P S E N S Q D L F P L A -

1501 CTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGT 1560  
F N L F C S D L R S Q I H L H K Y V V V -

1561 CTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTA 1620  
Y F R E I D T K D D Y N A L S V C P K Y -

1621 CCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGT 1680  
H L M K D A T A F C A E L L H V K Q Q V -

1681 GTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTGTAGCCCACCCA 1740  
S A G K R S Q A C H D G C C S L \*

1741 TGAGAAGCAAGAGACCTTAAAGGCTTCCTATCCCACCAATTACAGGGAAAAAACGTGTGA 1800

1801 TGATCCTGAAGCTTACTATGCAGCCTACAAACAGCCTTAGTAATTAAACATTTTATACC 1860

1861 AATAAAATTTTCAAATATTGCTAACTAATGTAGCATTAACTAACGATTGGAAACTACATT 1920

1921 TACAACCTTCAAAGCTGTTTTATACATAGAAATCAATTACAGCTTTAATTGAAAACGTGTA 1980

1981 CCATTTTGATAATGCAACAATAAAGCATCTTCAGC 2015

094093 034504  
094093 034504

**FIGURE 4**  
Homology of a Second IL-17 Human Receptor Like Polypeptide  
Amino Acid Sequence (SEQ ID No: 5) and KNown Human IL 17  
Receptor Family Mamber (SEQ ID NO: 3)

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1  MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRV 50
1  .....MGAARS 6
51  EPVTTSVATGDYSILMNVSWVLR.ADASIRLL.KATKICVTGKSNFQSYS 98
   |  .:|  :|:  ||  ||:|  :|  |
7   PP..SAVPGPLLGLLLLLLGV LAPGGASLRLLDHRALVCSQPGLNCTVKN 54
99  CVRLECSGAIMARCDLNLGSSDRSA.....SASRAAGTAGVGHQNWLI 142
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
55  STCLDDSW.IHPR...NLTPSSPKDLQIQLHFAHTQQGDLFPVAHIEWTL 100
143  ....FVVFVEGGFTVLLVLNSSAQAICL..PRLPKVL..GLQWTFYSYIGF 184
   :.:|  .|  ||..:|  |  |  |  |  |  |  |  |  |  |
101  QTDASILYLEGAELSVLQLNTN.ERLCVRFEFLSKLRHHHRRWRFTFSHF 149
185  PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKA 234
   |  :  |  :  |  |  |  |  |  |  |  |  |  |  |  |  |
150  VVDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSS 199
235  GSLWDPNITACKKNEETVEVNFTTTPLGNRYMALI.....QHSTIIGF 277
   |||||  |  |  |  |  |  |  |  |  |  |  |  |  |
200  GSLWDPNITVETLEAHQLRVSF TLWNESTHYQILLTSFPHMENHSCFEHM 249
278  SQVFEPHQKKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSDCIRHKG 324
   :  |  .  .  |  |  |  |  |  |  |  |  |  |  |  |  |
250  HHIPAPRPPEEFHQRSNVTLTLRNLKGCCRHQVQIQPFFSSCLNDCLRHSA 299
325  TVVLCPO.TGVPPFLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH 373
   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
300  T.VSCPEMPDTPEPIPDYMPLWVYWF.ITGISILLVGSVILLIVCMTWRL 347
374  ERIKTSFSFTTT.....LLP....PIKVLVVYPSE.ICFHHTICY 408
   :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
348  AGPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSADHPLYVDVVLK 397
409  FTEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK....KAADKVVFLL 454
   |  :|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
398  FAQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLC 447
455  SNDVNSVCDGTCGKSEGSP.....SENSQDLFPLAFNLFCSDLRSQIH 497
   |  .  .  |  |  |  |  |  |  |  |  |  |  |  |  |
448  SRGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPAC 495
498  LHKYVVVYFREIDTKDDY.NALSVC PKYHLMK..DATAFCAELLHVKKQV 544
   |||  ||  |  |  |  |  |  |  |  |  |  |  |  |  |
496  FGTYVVCYFSEVSCDGDVPDLFGAAPRYPLMDRFEEVYFRIQDLEMFPQG 545
545  SAGKRSQACHDGCCSL*..... 561
   :  :  |
546  RMHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECEENLYSADD 595

```

091002 03494  
 1267860

FIGURE 5  
Map of a Third IL-17 Receptor Like cDNA (SEQ ID NO: 6)  
and Amino Acid (SEQ ID NO: 7) Sequence

1 ATAAAAGCGCAGCGTGCGGGTGGCCTGGATCCCCGCGCAGTGGCCCGGCGATGTCGCTCGT 60  
61 GCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCGAGAGCCGACCGTTCAATG 120  
121 TGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCGGAGAGA 180  
181 CTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCAAT 240  
241 TTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGTGGACATTTTCCTACATCGGCTTCC 300  
M W T F S Y I G F P -  
301 CTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATATATTCCTAATGCAAATATGA 360  
V E L N T V Y F I G A H N I P N A N M N -  
361 ATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAA 420  
E D G P S M S V N F T S P G C L D H I M -  
421 TGAAATATAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTT 480  
K Y K K K C V K A G S L W D P N I T A C -  
481 GTAAGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAACCACTCCCCTGGGAAACAGAT 540  
K K N E E T V E V N F T T T P L G N R Y -  
541 ACATGGCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACC 600  
M A L I Q H S T I I G F S Q V F E P H Q -  
601 AGAAGAAACAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTA 660  
K K Q T R A S V V I P V T G D S E G A T -  
661 CGGTGCAGCTGACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAA 720  
V Q L T P Y F P T C G S D C I R H K G T -  
721 CAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGC 780  
V V L C P Q T G V P F P L D N N K S K P -  
781 CGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGG 840  
G G W L P L L L L S L L V A T W V L V A -  
841 CAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCA 900  
G I Y L M W R H E R I K K T S F S T T T -  
901 CACTACTGCCCCCATTAAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACA 960  
L L P P I K V L V V Y P S E I C F H H T -  
961 CAATTTGTTACTTCACTGAATTTCTTCAAAACCATTGCAGAAGTGAGGTCATCCTCGAAA 1020  
I C Y F T E F L Q N H C R S E V I L E K -  
1021 AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAAGA 1080  
W Q K K K I A E M G P V Q W L A T Q K K -  
1081 AGGCAGCAGACAAAGTCGTCTTCTTCTTCCAATGACGTCAACAGTGTGTGCGATGGTA 1140  
A A D K V V F L L S N D V N S V C D G T -  
1141 CCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCT 1200  
C G K S E G S P S E N S Q D L F P L A F -  
1201 TTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCACTCTGCACAAATACGTGGTGGTCT 1260  
N L F C S D L R S Q I H L H K Y V V V Y -  
1261 ACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACC 1320  
F R E I D T K D D Y N A L S V C P K Y H -



**THE**

**FIGURE 6**  
**Homology of a Third Human IL-17 Receptor Like Polypeptide**  
**Amino Acid Sequence (SEQ ID NO: 7) and Known Human IL-17**  
**Receptor Family Member (SEQ ID NO: 3)**

```

1 .....MWTFSYIGFP 10
      | | : |
101 QTDASILYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRRWRFTFSHFV 150
      .
11  VELNTVYFIGAHNIPNANMNEDGSPMSVNFTSPGCLDHIMKYKKKCVKAG 60
      | : . | : | : | . | | | | | | | | | | . . |
151 VDPDQEYEVTVHHLPKPIPDGDPNHQSKNFLVPDCEHARMKVTTPCMSSG 200
      .
61  SLWDPNITACKKNEETVEVNFTTTPLGNRYMALI .....QHSTIIGFS 103
      | | | | | | | | | | | | | | | | | | | | | |
201 SLWDPNITVETLEAHQLRVSF TLWNESTHYQILLTSFPHMENHSCFEHMH 250
      .
104 QVFEPHQKKQTRASVVIPVTGDSEGA...TVQLTPYFPTCGSDCIRHKGT 150
      : | | . . . | | . . | | : | : | . | . | : | | |
251 HIPAPRPEEFHQRSNVTLT LRNLKGCCR HQVQIQPFSSCLNDCLRHSAT 300
      .
151 VVLC PQ.TGV PFPLDNNSKPGGWLPLLLLSLLVATWVLVAGIYLMWRHE 199
      | | | : | | : . | : : | : | . | : . : : | |
301 .VSCPEMPDTPEPIPDY MPLWVYWF.ITGISILLVGSVILLIVCMTWRLA 348
      .
200 RIKKTSFSTTT .....LLP....PIKVLVVPSE.ICFHHTICYF 234
      : | | | | | | | | | | | | | | : : | : : : |
349 GPGSEKYSDDTKYTDGLPAADLIPPPLKPRKVWIIYSADHPLYVDVVLKF 398
      .
235 TEFLQNHCRSEVILEKWQKKKIAEMGPVQWLATQK...KAADKVVFLLS 280
      : | | | | . | | | : : . | . | | . | | | | : : | |
399 AQFLLTACGTEVALDLLEEQAISEAGVMTWVGRQKQEMVESNSKIIVLCS 448
      .
281 NDVNSVCDGTGCGKSEGPS .....SENSQDLFPLAFNLFCSDLRSQIHL 323
      . | : | . | | | | | | | | : | : |
449 RGTRAKWQALLGR..GAPVRLRCDHGKPVGDLFTAAMNMILPDFKRPACF 496
      .
324 HKYVVVYFREIDTKDDY.NALSVCPKYHLMK..DATAFCAELLHVKKQVS 370
      | | | | | | : | . | : | | | : | : | | . |
497 GTYVVCYFSEVSCDGDV PDLFGAAPRYPLMDRFEEVYFRIQDLEMFQPGR 546
      .
371 AGKRSQACHDGCCSL* ..... 386
      : : |
547 MHRVGELSGDNYLRSPGGRQLRAALDRFRDWQVRCPDWFECENLYSADDQ 596

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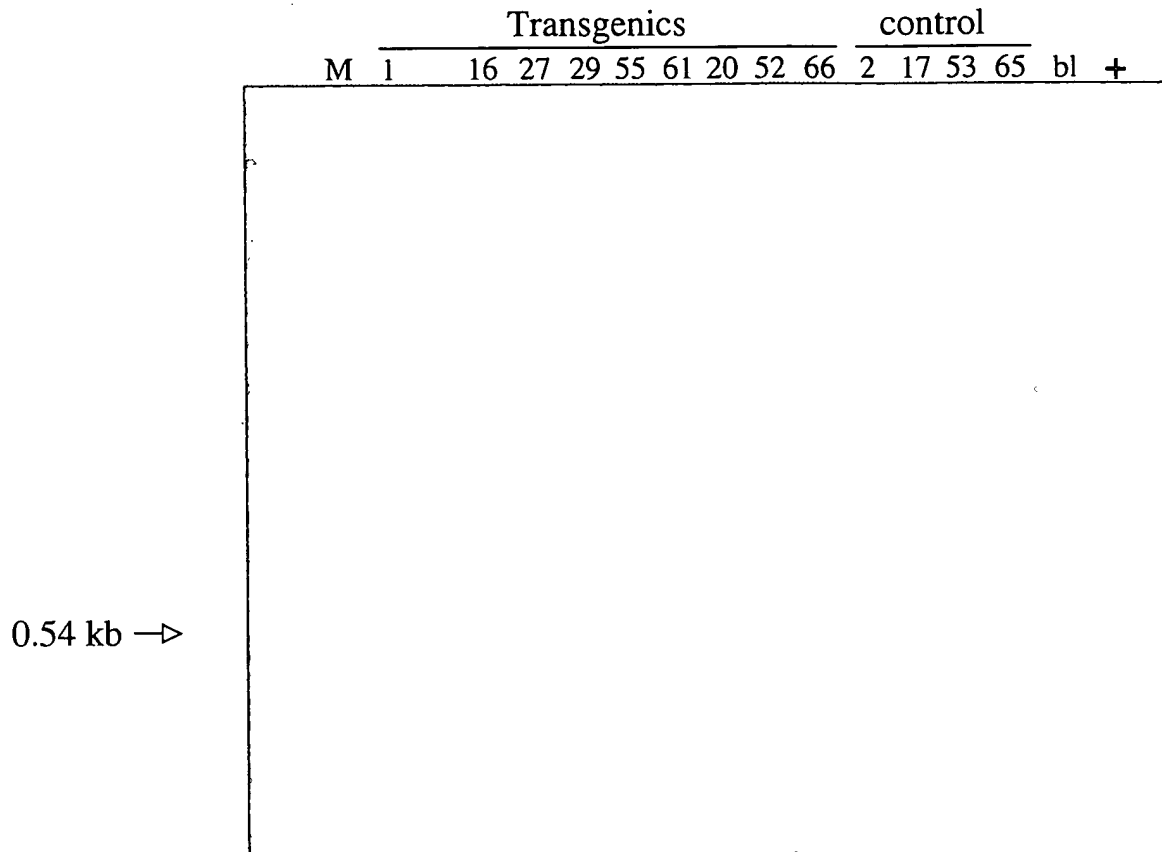
FIGURE 6

FIGURE 7  
Overlap of Amino Acid Sequences of the First (SEQ ID NO: 2),  
Second (SEQ ID NO: 5), and Third (SEQ ID NO: 7) Human IL-17  
Receptor Like Polypeptides

1	<b>MSLVLLSLAA</b>	LCSAVPREP	TVQCGSETGP	SPEWMLQHD	IPGDLRDLRV
1	<b>MSLVLLSLAA</b>	LCSAVPREP	TVQCGSETGP	SPEWMLQHD	IPGDLRDLRV
51	EPVTTSVATG	DYSILMNVS	WVLRADASIR	LKATKICVTG	KSNFQSYSCV
51	EPVTTSVATG	DYSILMNVS	WVLRADASIR	LKATKICVTG	KSNFQSYSCV
101	RCNYTEAFQT	QTRPSGGK--	-----	-----	-----
101	RLECSGAIMA	RCDLNLGSS	DRSASASRAA	GTVAGVGHQNW	LIFVVVFVEGG
119	-----	-----	-----WTFS	YIGFPVELNT	VYFIGAHNIP
151	FTVLLVLNSS	AQAICLPRLP	KVLGLQWTFS	YIGFPVELNT	VYFIGAHNIP
1			MWTFS	YIGFPVELNT	VYFIGAHNIP
143	NANMNEDGPS	MSVNFTSPGC	LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE
201	NANMNEDGPS	MSVNFTSPGC	LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE
26	NANMNEDGPS	MSVNFTSPGC	LDHIMKYKKK	CVKAGSLWDP	NITACKKNEE
193	TVEVNFTTTP	LGNRYMALIQ	HSTIIGFSQV	FEPHQKKQTR	ASVVIPVTGD
251	TVEVNFTTTP	LGNRYMALIQ	HSTIIGFSQV	FEPHQKKQTR	ASVVIPVTGD
76	TVEVNFTTTP	LGNRYMALIQ	HSTIIGFSQV	FEPHQKKQTR	ASVVIPVTGD
243	SEGATVQLTP	YFPTCGSDCI	RHKGTVVLC	QTVGPFFPLDN	NKSKPGGWLP
301	SEGATVQLTP	YFPTCGSDCI	RHKGTVVLC	QTVGPFFPLDN	NKSKPGGWLP
126	SEGATVQLTP	YFPTCGSDCI	RHKGTVVLC	QTVGPFFPLDN	NKSKPGGWLP
293	<u>LLLLSLLVAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTLLPPI</u>	<u>KVLVVYPSEI</u>
351	<u>LLLLSLLVAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTLLPPI</u>	<u>KVLVVYPSEI</u>
176	<u>LLLLSLLVAT</u>	<u>WVLVAGIYLM</u>	<u>WRHERIKKTS</u>	<u>FSTTLLPPI</u>	<u>KVLVVYPSEI</u>
343	CFHHTICYFT	EFLQNHCRSE	VILEKWQKKK	IAEMGPVQWL	ATQKKAADKV
401	CFHHTICYFT	EFLQNHCRSE	VILEKWQKKK	IAEMGPVQWL	ATQKKAADKV
226	CFHHTICYFT	EFLQNHCRSE	VILEKWQKKK	IAEMGPVQWL	ATQKKAADKV
393	VFLLSNDVNS	VCDGTCGKSE	GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK
451	VFLLSNDVNS	VCDGTCGKSE	GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK
276	VFLLSNDVNS	VCDGTCGKSE	GSPSENSQDL	FPLAFNLFCS	DLRSQIHLHK
443	YVVVYFREID	TKDDYNALSV	CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS
501	YVVVYFREID	TKDDYNALSV	CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS
326	YVVVYFREID	TKDDYNALSV	CPKYHLMKDA	TAFCAELLHV	KQQVSAGKRS
493	QACHDGCCSL	*			
551	QACHDGCCSL	*			
376	QACHDGCCSL	*			

Figure 8

# Northern Blot Expression Analysis of TH00-018 Necropsied Transgenic Founders



[illegible]

Figure 10

**Non-Transgenics**

**IL-17L Transgenics**

**A**

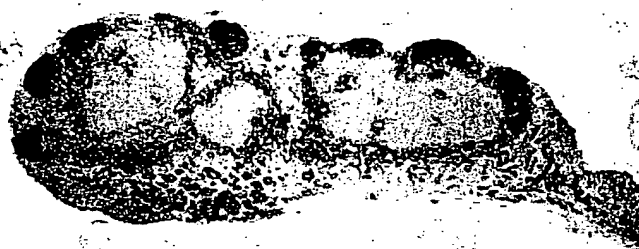


**Lymph Node H&E 2x**

**B**



**C**



**Lymph Node B220 2x**

**D**



**E**



**Lymph Node F4/80 2x**

**F**

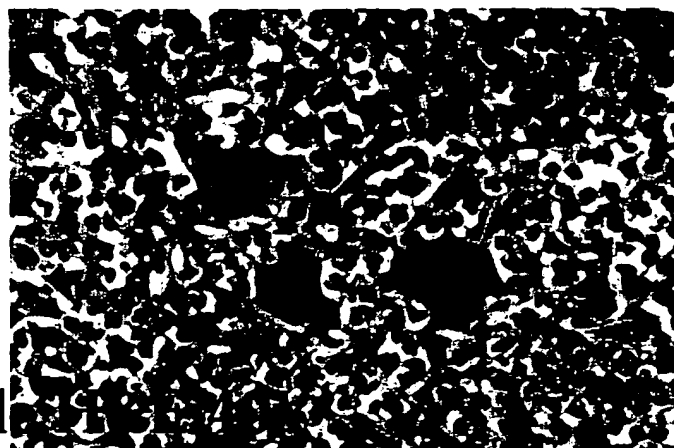
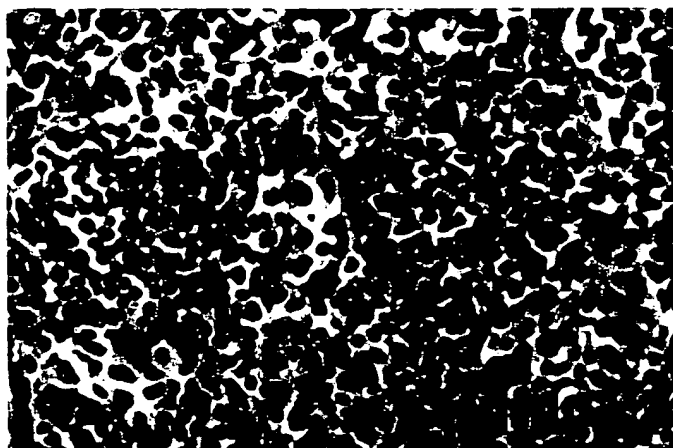
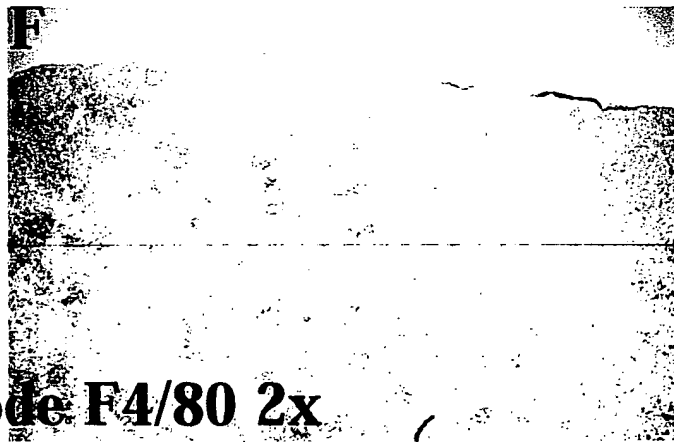
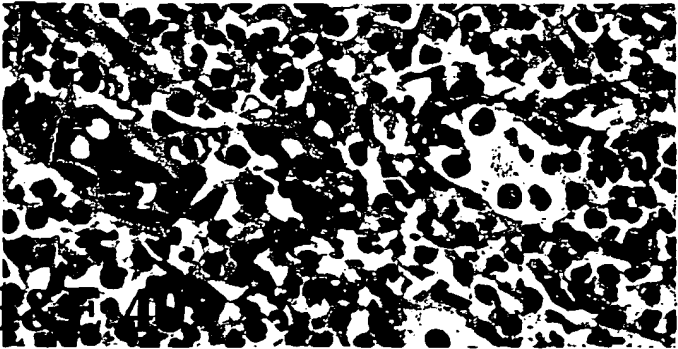
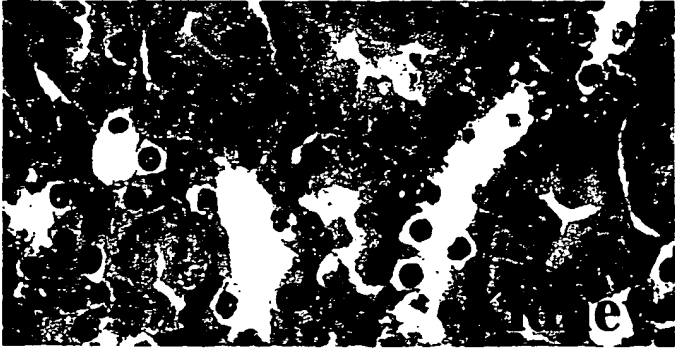
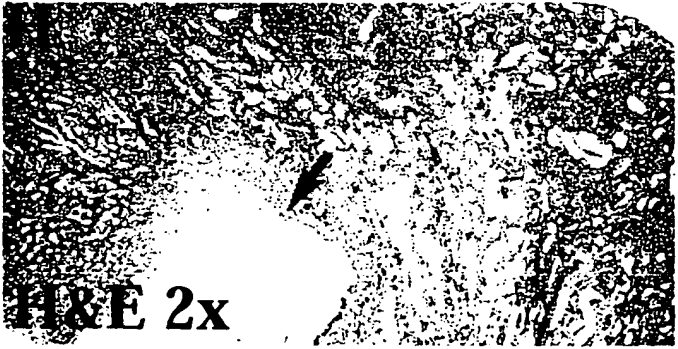
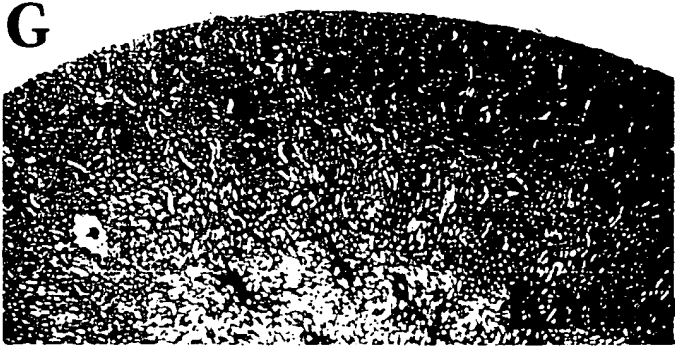
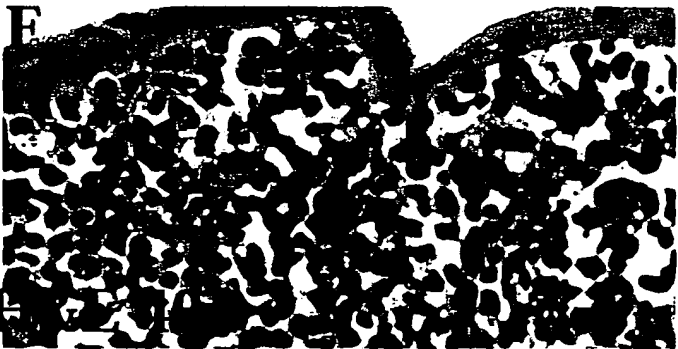
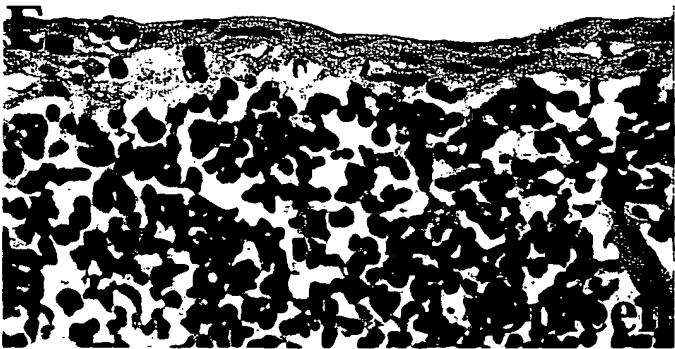
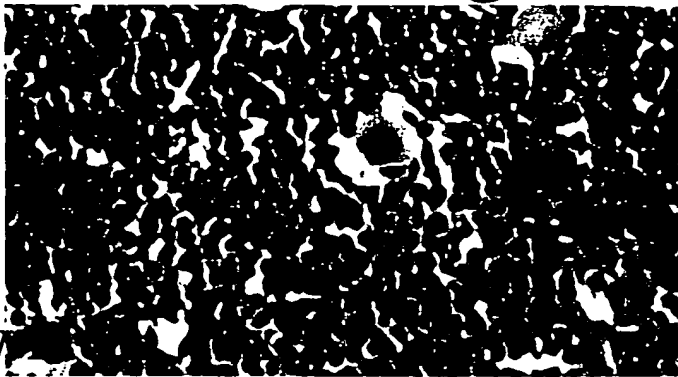
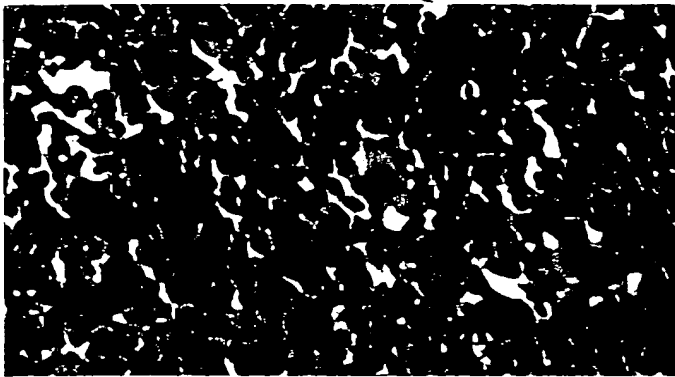


Figure 11

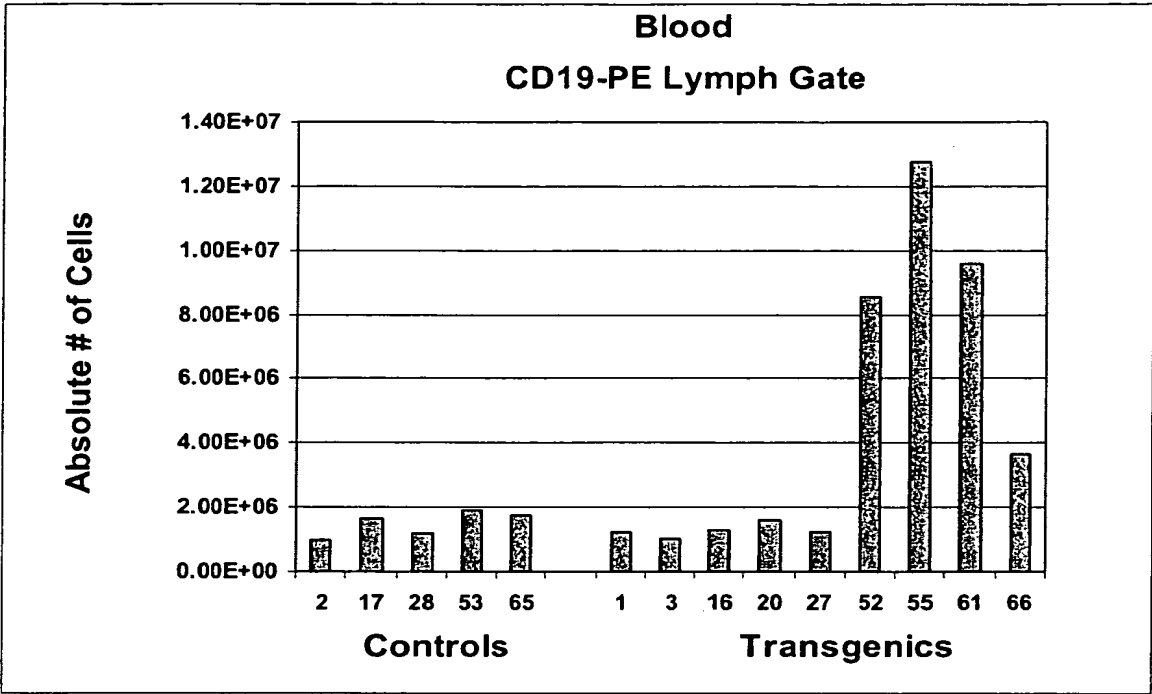
Non-Transgenics

IL-17<sup>T</sup> Transgenics



103120-20040403

Figure 12



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Figure 13

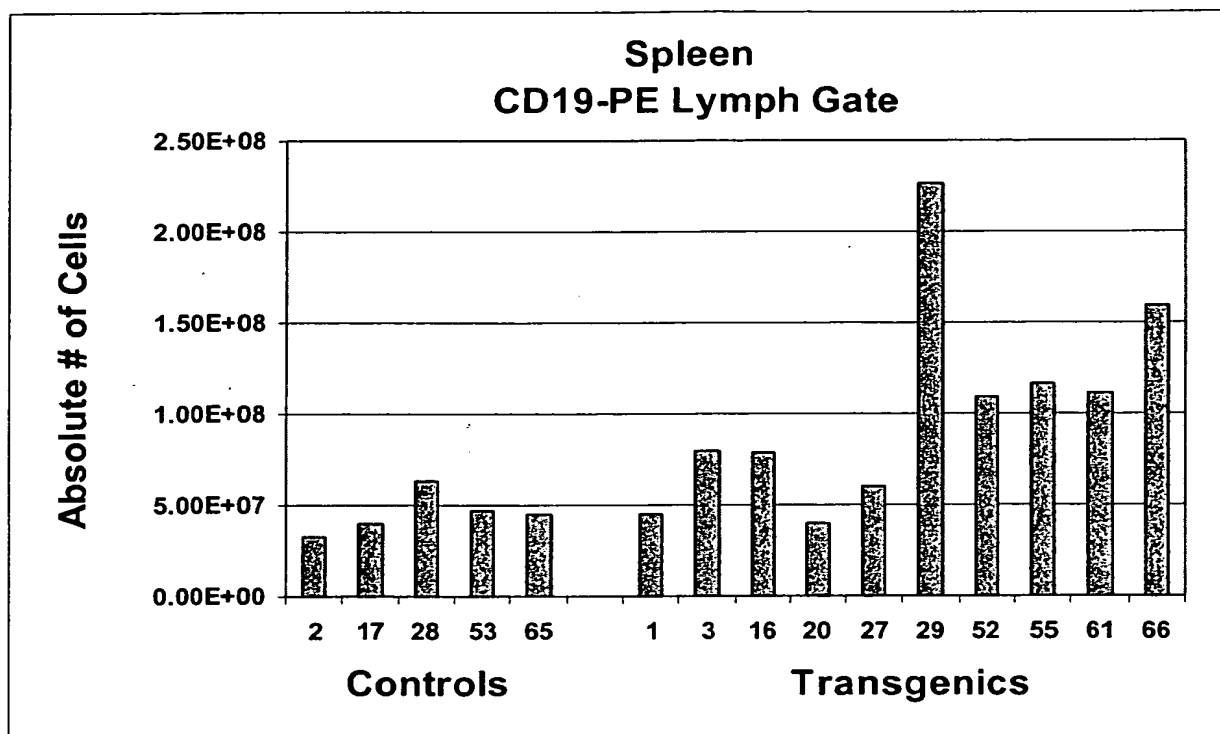


Figure 14

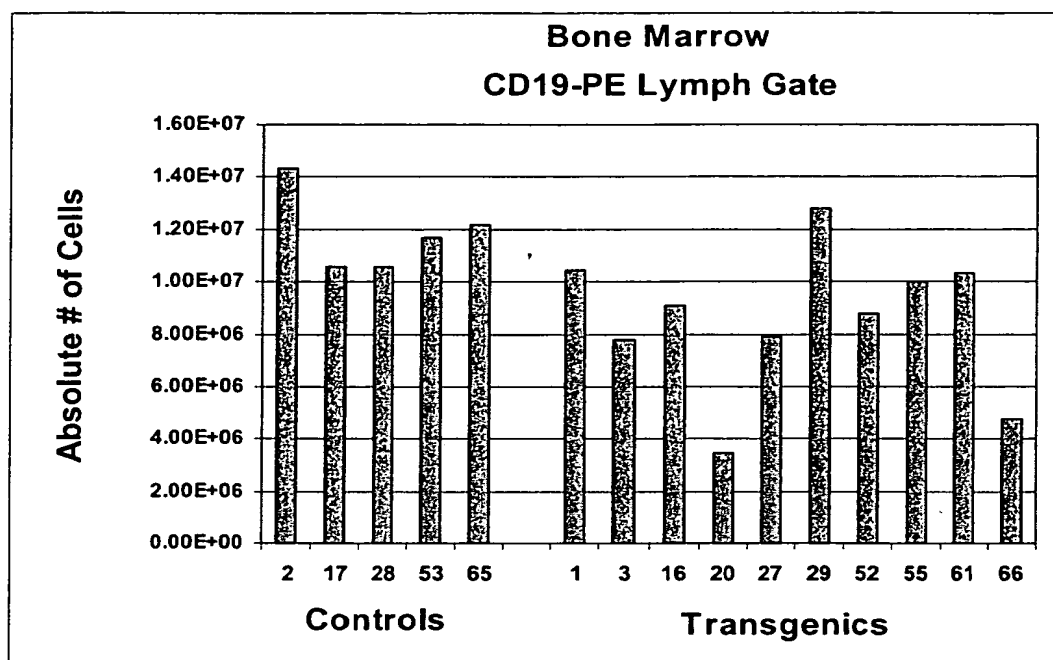
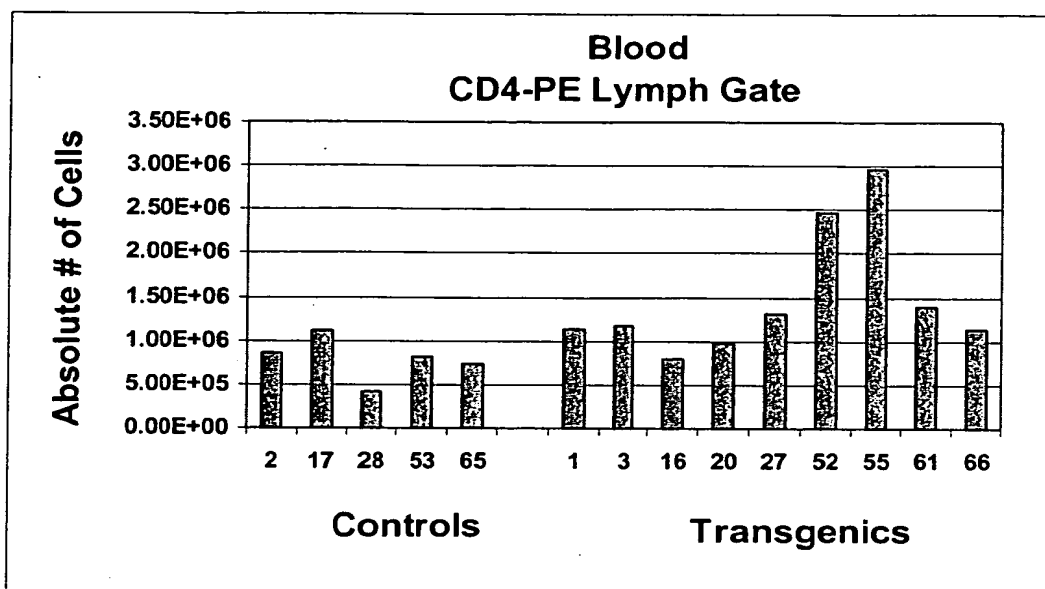


Figure 15



TOP SECRET

Figure 16

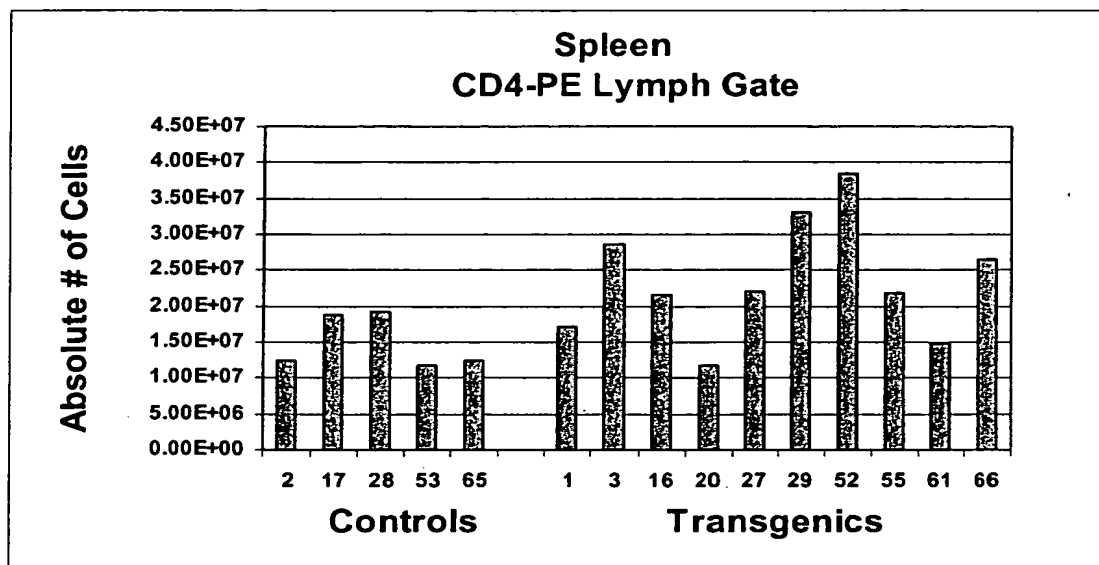


Figure 17

# CD45R+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW

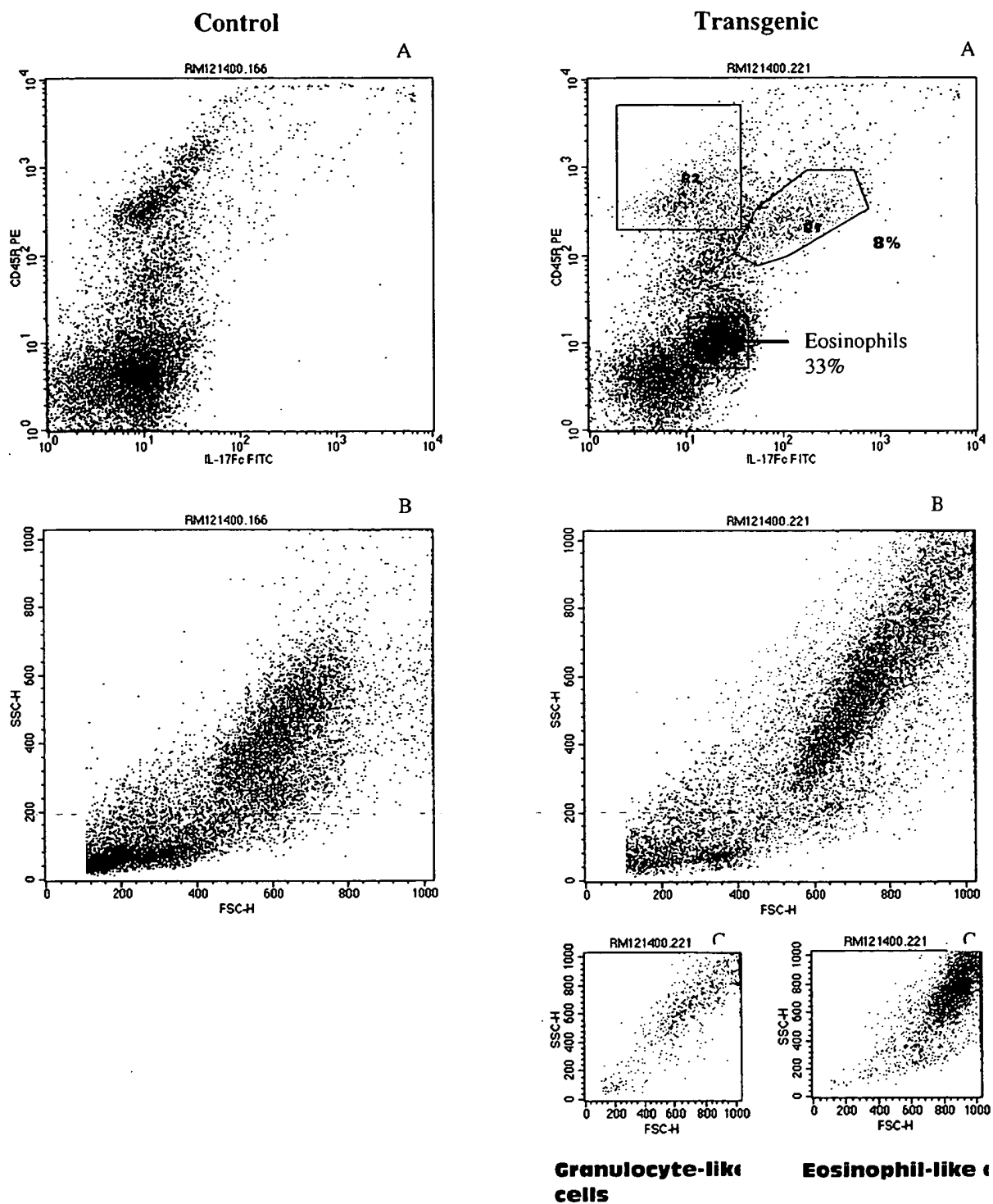


Figure 18

# CD4+ CELLS EXPRESSING IL17Br IN TRANSGENIC BONE MARROW

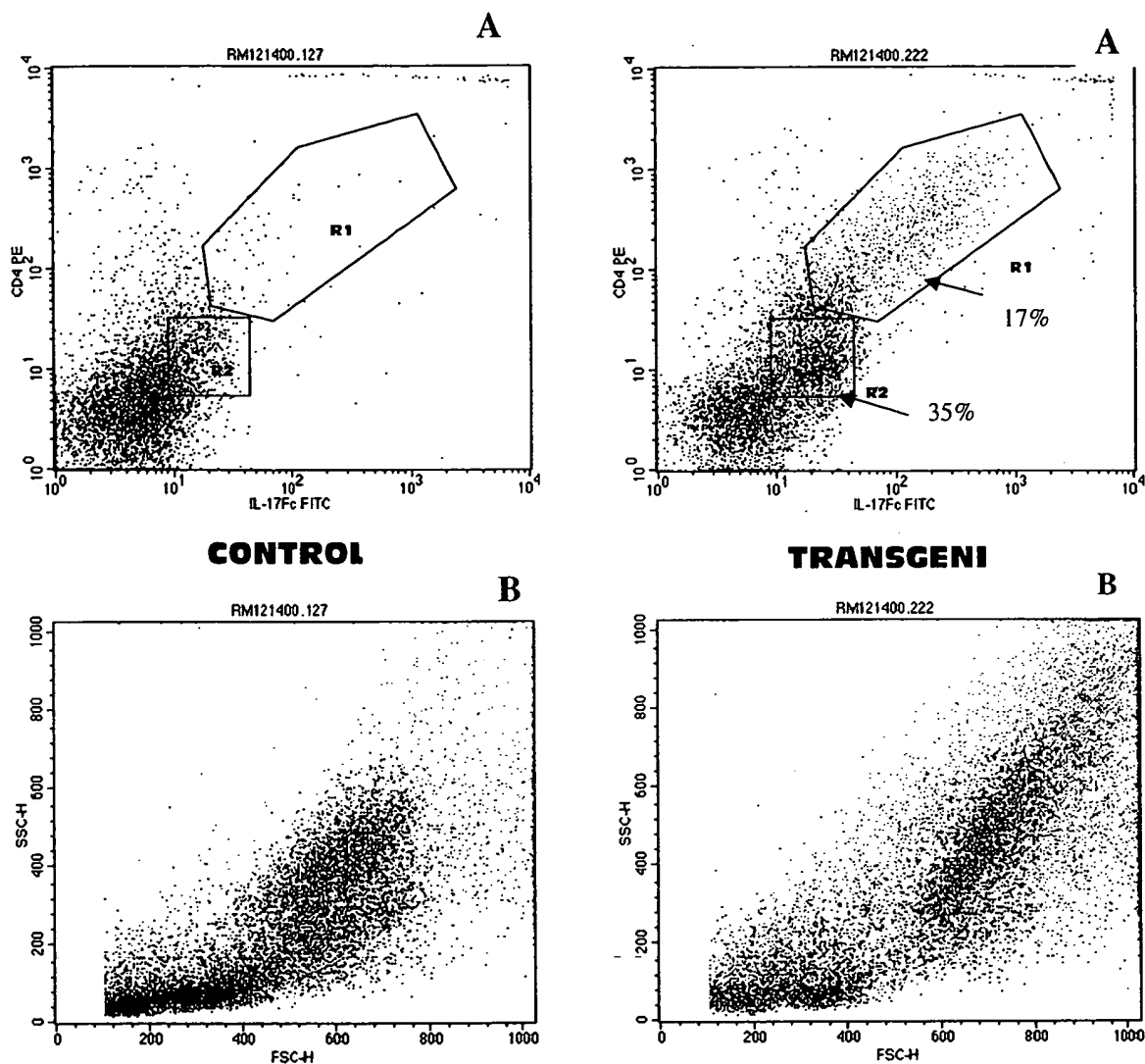
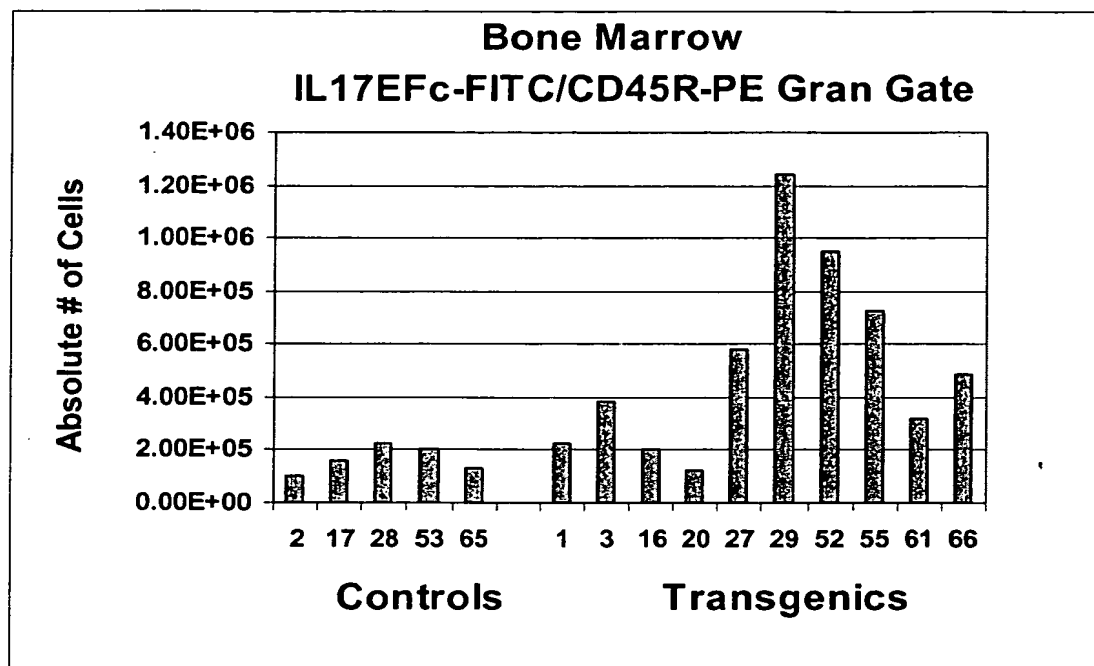
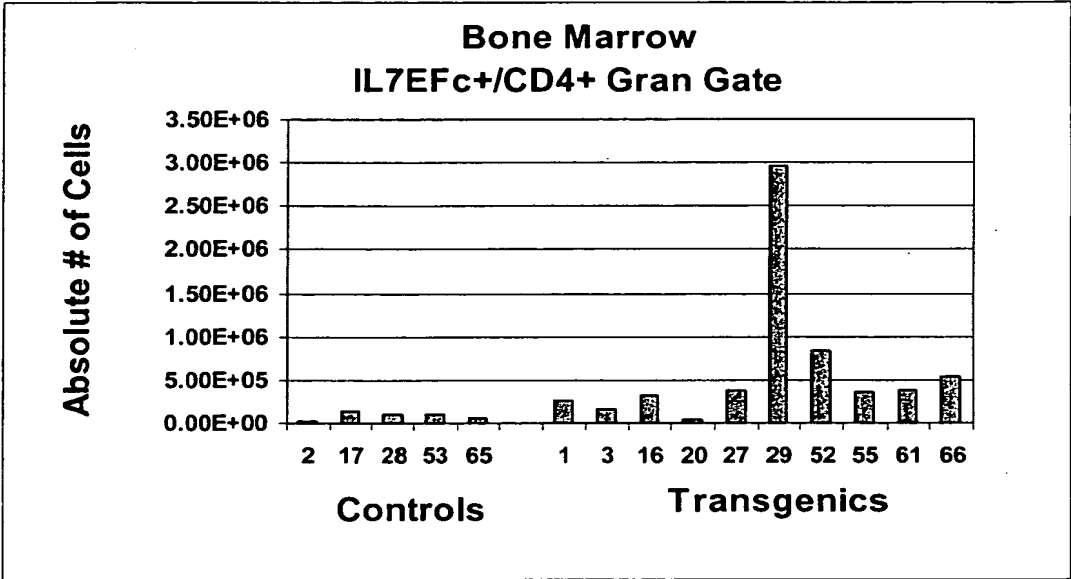


Figure 19



FOIA b 7 - 22501850

Figure 20



FOUO 22607850



Figure 21

Example of a typical eosinophil Forward vs. Side scatter plot (size vs. granularity). Cells in the gate can be sorted to give a purified population.

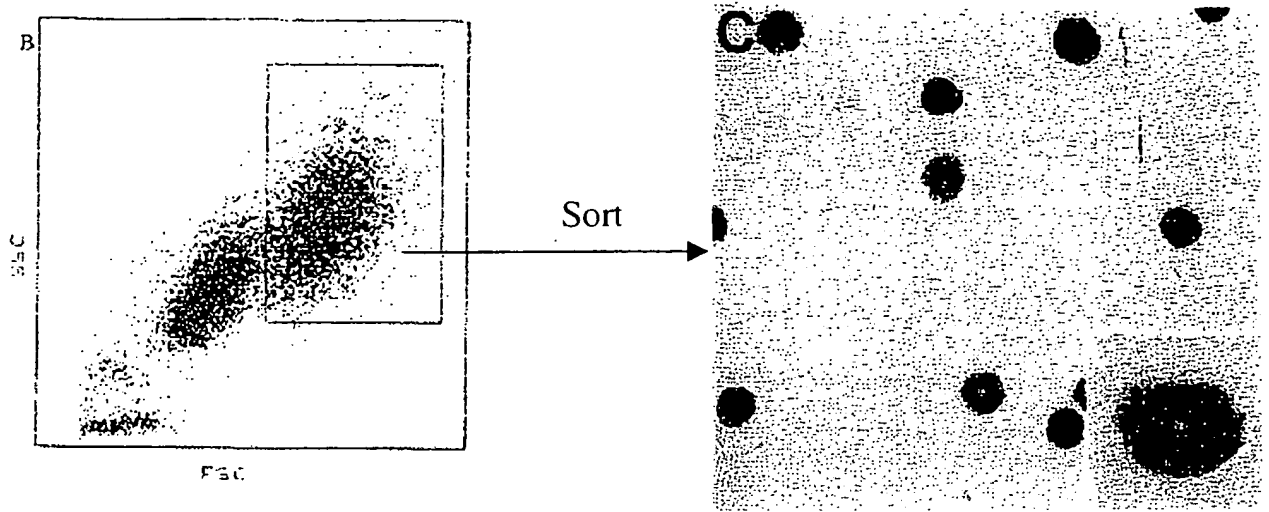


Figure 22

IL-17RB-2 Fusion Protein (SEQ ID NO: 24)

1    **MSLVLLSLAA** **LCRS**AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV  
51   EPVTTSVATG DYSILMNVS W VLRADASIRL LKATKICVTG KSNFQSYSCV  
101   RCNYTEAFQT QTRPSGGKWT FSYIGFPVEL NTVYFIGAHN IPNANMNEDG  
151   PSMSVNFTSP GCLDHIMKYK KKC VKAGSLW DPNITACKKN EETVEVNFTT  
201   TPLGNRYMAL IQHSTIIGFS QVFEPHQKKQ TRASVVIPVT GDSEGATVQL  
251   TPYFPTCGSD CIRHKGT VVL CPQTGVPFPL DNNKSKPGGW LPAAAEPKSC  
301   DKTHTCPPCP APELLGGPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED  
351   PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK  
401   CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLTCLVK  
451   GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL TVDKSRWQQG  
501   NVFSCSV MHE ALHNHYTQKS LSLSPGK\*

2025-09-22 10:24:00

Figure 23

Fusion Protein for IL-17RB-3 (SEQ ID NO: 25)

1    **MSLVLLSLAA** **LCRS**AVPREP TVQCGSETGP SPEWMLQHDL IPGDLRDLRV  
51   EPVTTSVATG DYSILMNVS W VLRADASIRL LKATKICVTG KSNFQSYSCV  
101   RLECSGAIMA RCDLNLLGSS DRSASASRAA GTAGVGHQTW LIFVVFVEGG  
151   FTVLLVLNSS AQAICLPRLP KVLGLQWTFS YIGFPVELNT VYFIGAHNIP  
201   NANMNEDGPS MSVNFTSPGC LDHIMKYKKK CVKAGSLWDP NITACKKNEE  
251   TVEVNFTTTP LGNRYMALIQ HSTIIGFSQV FEPHQKKQTR ASVVIPVTGD  
301   SEGATVQLTP YFPTCGSDCI RHKGTVVLCP QTGVPPPLDN NKSKPGGWLP  
351   AAAEPKSCDK THTCPPCPAP ELLGGPSVFL FPPKPKDTLM ISRTPEVTCV  
401   VVDVSHEDPE VKFNWYVDGV EVHNAKTKPR EEQYNSTYRV VSVLTVLHQD  
451   WLNKEYKCK VSNKALPAPI EKTISKAKGQ PREPQVYTL PSRDELTKNQ  
501   VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPVLDSDG SFFLYSKLTV  
551   DKSRWQQGNV FSCSVMEAL HNHYTQKSLS LSPGK\*

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